

STIC-Biotech/Ch mLib

85933

From: Schultz, James
Sent: Tuesday, February 04, 2003 10:18 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 09/960,143

12E18

Hello,
Could you please run a length limited nucleotide sequence search on SEQ ID NO:3 (1639 nt long) in the above entitled application, where the maximum size of the returned hits are no longer than 50 nucleotides?
Thanks,
Doug Schultz

J. Douglas Schultz, Ph.D.
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(703) 308-9355
(703) 746-3973 (fax)
Office: CM1 12E18
Mail: CM1 11E12

CARE

Point of Contact:
Thomas G. Larson, Ph.D.
703-308-7309
CM1, Rm. 6 B 01

Searcher: Larson
Phone: _____
Location: _____
Date Picked Up: 2/4
Date Completed: 2/13
Searcher Prep/Review: 10
Clerical: _____
Online time: 5

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: ABSS03
WWW/Internet: _____
Other (specify): _____

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Result No.	Score	Query %		Length	DB	ID	Description
		Match	Match				
C 1	37.4	2.3	47	1	US-08-330-163-42	Sequence 42, Appl	
C 2	37.4	2.3	47	1	US-08-482-111-42	Sequence 42, Appl	
C 3	37	2.3	37	1	US-08-330-163-40	Sequence 40, Appl	
C 4	37	2.3	37	1	US-08-482-111-40	Sequence 40, Appl	
C 5	33	2.0	33	2	US-08-410-654B-42	Sequence 42, Appl	
C 6	33	2.0	33	2	US-08-47A-851-42	Sequence 42, Appl	
C 7	33	2.0	33	2	US-08-481-860-42	Sequence 42, Appl	
C 8	31	1.9	31	5	PCT-US96-08142-9	Sequence 9, Appl	
C 9	30	1.8	30	4	US-09-308-160B-6	Sequence 6, Appl	
C 10	30	1.8	30	4	US-09-456-399-6	Sequence 6, Appl	
C 11	28	1.7	28	2	US-08-859-998-479	Sequence 479, Appl	
C 12	28	1.7	28	2	US-08-859-998-480	Sequence 480, Appl	
C 13	28	1.7	28	4	US-09-235-928-479	Sequence 479, Appl	
C 14	28	1.7	28	4	US-09-235-928-480	Sequence 480, Appl	
C 15	25	1.5	25	1	US-08-327-494A-8	Sequence 8, Appl	
C 16	25	1.5	25	5	PCT-US95-13659-8	Sequence 8, Appl	
C 17	25	1.5	25	5	PCT-US96-08142-8	Sequence 8, Appl	
C 18	24	1.5	24	4	US-09-710-200-72	Sequence 8, Appl	
C 19	24	1.5	24	5	PCT-US96-08142-7	Sequence 72, Appl	
C 20	23.4	1.4	47	4	US-09-641-638-1167	Sequence 7, Appl	
C 21	23	1.4	23	5	US-08-327-494A-7	Sequence 1167, Ap	
C 22	23	1.4	23	5	PCT-US95-13659-7	Sequence 7, Appl	
C 23	23	1.4	40	1	US-08-482-111-53	Sequence 7, Appl	
C 24	22	1.3	22	4	US-09-046-894-20	Sequence 53, Appl	
C 25	22	1.3	48	1	US-08-317-102-1	Sequence 20, Appl	
C 26	21.8	1.3	47	4	US-09-338-907-250	Sequence 1, Appl	
C 27	21.8	1.3	47	4	US-09-338-907-327	Sequence 250, App	
						Sequence 327, App	

RESULT 3
 US-08-330-163-40/c
 Sequence No. Application US/08330163
 Patent No. 565672A
 GENERAL INFORMATION:
 APPLICANT: Daly, Thomas J.
 APPLICANT: LaRosa, Gregory J.
 TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
 TITLE OF INVENTION: Use
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA: US/08/482,111
APPLICATION NUMBER: 07-JUN-1995
FILING DATE: 514
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 00231/083001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
482-111-40

Query Match 2.38; Score 37; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 18;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 GGTGTGGAGAGCTTTTGAAGAGGGCTGAGAAATTC 387
Db 37 GGTGTGGAGAGCTTTTGAAGAGGGCTGAGAAATTC 1

RESULT 5

US-08-410-654B-42/c
Sequence 42, Application US/08410654B
Patent No. 5833976
GENERAL INFORMATION:
APPLICANT: Rene de Waal Malefyt
APPLICANT: Di-Hwei Hsu
APPLICANT: Anne O'Garra
APPLICANT: Hergen Spits
TITLE OF INVENTION: Use of Interleukin-10 to Treat
TITLE OF INVENTION: Septic Shock
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,654B
FILING DATE: 24-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-410-654B-42

Query Match 2.0%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
Db 33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1

RESULT 6

US-08-410-851-42/c
Sequence 42, Application US/08474851
Patent No. 5837232
GENERAL INFORMATION:

APPLICANT: Rene de Waal Malefyt
APPLICANT: Di-Hwei Hsu
APPLICANT: Anne O'Garra
APPLICANT: Hergen Spits
TITLE OF INVENTION: Use of An Interleukin-10 Antagonist to Treat
TITLE OF INVENTION: A B Cell Mediated Autoimmune Disorder
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,851
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,654
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1GID
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-474-851-42

Query Match 2.0%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
Db 33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1

RESULT 7

US-08-481-560-42/c
Sequence 42, Application US/08481560
Patent No. 5837293
GENERAL INFORMATION:

APPLICANT: Rene de Waal Malefyt
APPLICANT: Di-Hwei Hsu
APPLICANT: Anne O'Garra
APPLICANT: Hergen Spits
TITLE OF INVENTION: Use of Interleukin-10 to Modulate
TITLE OF INVENTION: Inflammation or T-Cell Mediated
TITLE OF INVENTION: Immune Function
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road

;; PRIOR APPLICATION NUMBER: PCT/JP97/04127
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: US 09/308,160
;; PRIOR FILING DATE: 1999-05-14
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 30
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: an artificially
;; OTHER INFORMATION: synthesized primer sequence
US-09-456-399-6

Query Match 1.8%; Score 30; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GACAGCAGCAGCACACAGCTTCTAGGACAA 43
|||||
Db 30 GACAGCAGCAGCACACAGCTTCTAGGACAA 1

RESULT 11
US-08-859-998-479
; Sequence 479, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 479:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-479

Query Match 1.7%; Score 28; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 88 AACATGACITTCACAGCTGGCGGTGGCTC 115
|||||
Db 1 AACATGACITTCACAGCTGGCGGTGGCTC 28

RESULT 12
US-08-859-998-480/c
; Sequence 480, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 480:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-480

Query Match 1.7%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 GAGTGATTGAGAGTGACACACACTGCCG 275
|||||
Db 28 GAGTGATTGAGAGTGACACACACTGCCG 1

RESULT 13
US-09-225-928-479
; Sequence 479, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvilli, Robert


```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-327-494A-8

Query Match          1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAAGTTTTTGAAGGGCTGAGA 382
Db 25 GAGAAGTTTTTGAAGGGCTGAGA 1

RESULT 16
PCT-US95-13659-8/c
Sequence 8, Application PC/TUS9513659
GENERAL INFORMATION:
APPLICANT: Blaser, Martin J.
APPLICANT: Tumuru, Murali K.R.
APPLICANT: Sharma, Smita A
TITLE OF INVENTION: cagB and cagC Genes for H. pylori and
TITLE OF INVENTION: Related Methods and Compositions
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 303-3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13659
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 2200.029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-13659-8

Query Match          1.5%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAAGTTTTTGAAGGGCTGAGA 382
Db 25 GAGAAGTTTTTGAAGGGCTGAGA 1

RESULT 17
PCT-US96-08142-8/c
Sequence 8, Application PC/TUS9608142
GENERAL INFORMATION:
APPLICANT: Constance Emmett, Kimberly A. Foster
TITLE OF INVENTION: Universal Chemistry Enzyme-Linked
TITLE OF INVENTION: Immunosorbent Assay for Detection of
TITLE OF INVENTION: mRNA Expression
```

```

; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08142
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: TCEL-0039
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
PCT-US96-08142-8

Query Match          1.5%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAAGTTTTTGAAGGGCTGAGA 382
Db 25 GAGAAGTTTTTGAAGGGCTGAGA 1

RESULT 18
US-09-710-200-72/c
Sequence 72, Application US/09710200
GENERAL INFORMATION:
APPLICANT: Nanogen, Inc.
APPLICANT: Weidenhammer, Elaine M.
APPLICANT: Wang, Ling
APPLICANT: Xu, Xiao
APPLICANT: Heller, Michael J.
APPLICANT: Kahl, Brenda F.
TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
FILE REFERENCE: 256/262 Patrick S. Eagelman
CURRENT APPLICATION NUMBER: US/09/710,200
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 72
LENGTH: 24
TYPE: DNA
ORGANISM: Homo sapiens
US-09-710-200-72

Query Match          1.5%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 GTCTGGGCTCTGTTGTAGGTTGCC 498
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Db 24 GTGTGGCTGTCTGTAGGGTGGCC 1
|||||
PCT-US96-08142-7
Sequence 7, Application PC/TUS9608142
GENERAL INFORMATION:
APPLICANT: Constance Emmett, Kimberly A. Foster
TITLE OF INVENTION: Universal Chemistry Enzyme-Linked
TITLE OF INVENTION: Immunosorbent Assay for Detection of
TITLE OF INVENTION: mRNA Expression
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08142
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: TCEL-0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No
PCT-US96-08142-7

Query Match 1.5%; Score 24; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 ATGACTTCCAAGCTGGCGCTGGCT 114
Db 1 ATGACTTCCAAGCTGGCGCTGGCT 24
|||||
RESULT 20
US-09-641-638-1167/c
Sequence 1167, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11

Query Match 1.4%; Score 23.4; DB 4; Length 47;
Best Local Similarity 69.8%; Pred. No. 1.1e+04;
Matches 30; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1256 AACAAATAATTTTCTACTATAAGTACATTATTGTTTATCTGAA 1298
Db 46 AAAAAATAATTAATAAGAAAGAAAAAACTGTCTTCTCATCTGAA 4
|||||
Search completed: February 9, 2003, 19:22:03
Job time : 103 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 17:25:52 : Search time 133 seconds
(without alignments)
5841.285 Million cell updates/sec

Title: US-09-960-143-3
Perfect score: 1639
Sequence: 1 acaacttcagacagca.....ataaattgttgcagaagt 1639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 231544

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.6	1.9	31	10	US-09-801-274-1358
C 2	30	1.8	30	10	US-09-816-124-4
C 3	25	1.5	25	10	US-09-885-441-31
C 4	24	1.5	24	10	US-09-975-408-72
C 5	24	1.5	24	12	US-10-075-579-72
C 6	21.8	1.3	47	9	US-09-853-526-250
C 7	21.8	1.3	47	9	US-09-853-526-327
C 8	21.8	1.3	47	10	US-09-901-484A-250
C 9	21.8	1.3	47	10	US-09-901-484A-327
10	21.6	1.3	41	10	US-09-955-462A-1
11	20.4	1.2	34	10	US-09-955-462A-2
12	20.4	1.2	48	9	US-09-864-785-3472
13	20.2	1.2	48	9	US-09-864-785-3568
C 14	20	1.2	20	10	US-09-975-408-73
C 15	20	1.2	20	12	US-10-075-579-73
C 16	20	1.2	28	10	US-09-142-593-40
C 17	20	1.2	48	9	US-09-864-785-3460
18	19.8	1.2	43	9	US-09-828-523A-96
19	19.8	1.2	48	9	US-09-825-805-64

C	20	19.6	1.2	45	9	US-10-017-736-9	Sequence 9, Appli
	21	19.4	1.2	49	10	US-09-773-385-3	Sequence 3, Appli
	22	19.4	1.2	50	9	US-09-992-598-45	Sequence 45, Appl
	23	19.4	1.2	50	9	US-09-989-293A-45	Sequence 45, Appl
	24	19.4	1.2	50	9	US-09-989-735-45	Sequence 45, Appl
	25	19.4	1.2	50	9	US-09-990-444-45	Sequence 45, Appl
	26	19.4	1.2	50	9	US-09-989-730-45	Sequence 45, Appl
	27	19.4	1.2	50	9	US-09-990-436-45	Sequence 45, Appl
	28	19.4	1.2	50	9	US-09-991-181-45	Sequence 45, Appl
	29	19.4	1.2	50	9	US-09-993-687-45	Sequence 45, Appl
	30	19.4	1.2	50	9	US-09-989-734-45	Sequence 45, Appl
	31	19.4	1.2	50	9	US-09-997-653-45	Sequence 45, Appl
	32	19.4	1.2	50	9	US-09-993-667-45	Sequence 45, Appl
	33	19.4	1.2	50	10	US-09-989-722-45	Sequence 45, Appl
	34	19.4	1.2	50	10	US-09-989-723-45	Sequence 45, Appl
	35	19.4	1.2	50	10	US-09-989-279-45	Sequence 45, Appl
	36	19.4	1.2	50	10	US-09-989-727-45	Sequence 45, Appl
	37	19.4	1.2	50	10	US-09-989-731-45	Sequence 45, Appl
	38	19.4	1.2	50	10	US-09-989-732-45	Sequence 45, Appl
	39	19.4	1.2	50	10	US-09-991-073-45	Sequence 45, Appl
	40	19.4	1.2	50	10	US-09-990-442-45	Sequence 45, Appl
	41	19.4	1.2	50	10	US-09-991-163-45	Sequence 45, Appl
	42	19.4	1.2	50	10	US-09-993-604-45	Sequence 45, Appl
	43	19.4	1.2	50	10	US-09-990-456-45	Sequence 45, Appl
	44	19.4	1.2	50	10	US-09-989-721-45	Sequence 45, Appl
	45	19.2	1.2	24	10	US-09-885-441-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-801-274-1358
; Sequence 1358, Application US/09801274
; Patent No. US2002032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1358
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1358

Query Match 1.9%; Score 30.6; DB 10; Length 31;
Best Local Similarity 96.8%; Pred. No. 2.4e+03;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 220 TTCCACCCCAATTTATCAAGAACTGAGAG 250
Db 1 TTCCACCCCAATTTATCAAGAACTGAGAG 31

RESULT 2
US-09-816-124-4
; Sequence 4, Application US/09816124
; Patent No. US20020150897A1
; GENERAL INFORMATION:
; APPLICANT: Nagasawa, Yasuo
; APPLICANT: Yoshida, Hideaki
; TITLE OF INVENTION: Method for detecting and isolating genes
; FILE REFERENCE: SI-801PCT

; CURRENT APPLICATION NUMBER: US/09/816.124
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: PCT/JP97/04126
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JP 1996-305163
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence
US-09-816-124-4

Query Match 1.8%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GACAGCAGACACACAAAGCTTCTAGGACAA 43
|||||
Db 30 GACAGCAGACACACAAAGCTTCTAGGACAA 1

RESULT 3
US-09-885-441-31/c
; Sequence 31 Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885.441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212.844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244.171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279.766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 31
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-885-441-31

Query Match 1.5%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 888 TGTTCCACTGCGCTGGTTCTCC 912
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Db 25 TGTTCCACTGCGCTGGTTCTCC 1

RESULT 4
US-09-975-408-72/c
; Sequence 7 Application US/09975408
; Patent No. US20020150917A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Xu, Xiao
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MIC
; FILE REFERENCE: 267/174 Patrick S. Eaglenan
; CURRENT APPLICATION NUMBER: US/09/975.408

; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/710.200
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-975-408-72

Query Match 1.5%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 475 GTGTGGGTCTGTGTAGGGTTGCC 498
|||||
Db 24 GTGTGGGTCTGTGTAGGGTTGCC 1

RESULT 5
US-10-075-579-72/c
; Sequence 72 Application US/10075579
; Patent No. US20020119484A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Wang, Ling
; APPLICANT: Xu, Xiao
; APPLICANT: Heller, Michael J.
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
; FILE REFERENCE: 256/262 Patrick S. Eaglenan
; CURRENT APPLICATION NUMBER: US/10/075.579
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/710.200
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-075-579-72

Query Match 1.5%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 475 GTGTGGGTCTGTGTAGGGTTGCC 498
|||||
Db 24 GTGTGGGTCTGTGTAGGGTTGCC 1

RESULT 6
US-09-853-526-250/c
; Sequence 250 Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET 18CPICP
; CURRENT APPLICATION NUMBER: US/09/853.526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338.907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996.306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099.658
; PRIOR FILING DATE: 1998-09-09

QY 1038 TATTATTATTATGTATTATTAAAGC 1065

QY 1038 TATTATTATTATGTATTATTAAAGC 1065

RESULT 13
US-09-864-785-3568

RESULT 13
US-09-864-785-3568

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; Sequence 3568, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McGwaggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3568
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-3568

Query Match 1.2%; Score 20.2; DB 9; Length 48;
Best Local Similarity 63.4%; Pred. No. 1.7e+05;
Matches 26; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 12 GAGACAGCAGACACACAGCTTCTAGGACAGAGCCAGGA 52
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 41

RESULT 14
US-09-975-408-73/c
; Sequence 73, Application US/09975408
; Patent No. US20020150917A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Xu, Xiao
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MIC
; FILE REFERENCE: 267/174 Patrick S. Eagleman
; CURRENT APPLICATION NUMBER: US/09/975,408
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/710,200
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-09-975-408-73

Query Match 1.2%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGAAGTTTTTGAAGAGGGCT 378
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Db 20 AGAAGTTTTTGAAGAGGGCT 1

RESULT 15
US-10-075-579-73/c
; Sequence 73, Application US/10075579
; Patent No. US2002011948A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
```

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; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Wang, Ling
; APPLICANT: Xu, Xiao
; APPLICANT: Heller, Michael J.
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
; FILE REFERENCE: 256/262 Patrick S. Eagleman
; CURRENT APPLICATION NUMBER: US/10/075,579
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/710,200
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-10-075-579-73

Query Match 1.2%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGAAGTTTTTGAAGAGGGCT 378
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 AGAAGTTTTTGAAGAGGGCT 1

RESULT 16
US-09-142-593-40/c
; Sequence 40, Application US/09142593
; Patent No. US20020016975A1
; GENERAL INFORMATION:
; APPLICANT: HACKETT ET AL.
; TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESS: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,593
; FILING DATE: 10-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/040,564
; FILING DATE: 11-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,868
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/065,303
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/04687
; FILING DATE: 11-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 110.00450101
```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1226
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-142-593-40

Query Match 1.2%; Score 20; DB 10; Length 28;

Best Local Similarity 82.1%; Pred. No. 1.7e+05;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 75 CTCACGTGTGTAAACATGACTTCCAAAG 102

Db 28 CTTATTGTATGTAACCTTGACTTTCAG 1

RESULT 17

US-09-864-785-3460

Sequence 3460, Application US/09864785

Patent No. US20020177568A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Stinchcomb, Dan

APPLICANT: Draper, Ken

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to

TITLE OF INVENTION: Levels of NF-Kappa B

FILE REFERENCE: 400/022 (MBH00-812-D)

CURRENT APPLICATION NUMBER: US/09/864,785

CURRENT FILING DATE: 2001-05-23

NUMBER OF SEQ ID NOS: 3929

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3460

LENGTH: 48

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-864-785-3460

Query Match 1.2%; Score 20; DB 9; Length 48;

Best Local Similarity 61.4%; Pred. No. 1.9e+05;

Matches 27; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

QY 13 AGACAGCAGCAGCACAAAGCTTCTAGGACAGAGCCGAGGAAGAA 56

Db 2 AGACUCCGGAGGAACUCCUUCUACAGGACACUCCGCGGACAAA 45

RESULT 18

US-09-828-523A-96

Sequence 96, Application US/09828523A

Patent No. US20020168697A1

GENERAL INFORMATION:

APPLICANT: The Pharmacia & Upjohn Company

TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS

FILE REFERENCE: 268.62120101

CURRENT APPLICATION NUMBER: US/09/828,523A

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/266,327

PRIOR FILING DATE: 2000-04-06

NUMBER OF SEQ ID NOS: 99

SOFTWARE: PatentIn version 3.1

SEQ ID NO 96

LENGTH: 43

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide Primer.

US-09-828-523A-96

Query Match 1.2%; Score 19.8; DB 9; Length 43;

Best Local Similarity 69.2%; Pred. No. 2e+05;

Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 612 ATCTACAAAAACAATAATTTTGAATATAAGGAT 650

Db 4 ATCTGCAATAATATCTTTTAAATTTTAAATTTAAAGAAAT 42

RESULT 19

US-09-825-805-64

Sequence 64, Application US/09825805

Publication No. US20030004122A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Beigelman, Leo

APPLICANT: Beaudry, Amber

APPLICANT: Karpeisky, Alex

APPLICANT: Adamic, Jasenka Matulic

APPLICANT: Sweedler, Dave

APPLICANT: Zinnen, Shawn

TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides

FILE REFERENCE: MBH00-831-F (400/009)

CURRENT APPLICATION NUMBER: US/09/825,805

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/578,223

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 09/476,387

PRIOR FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: 09/474,432

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/301,511

PRIOR FILING DATE: 1999-04-28

PRIOR APPLICATION NUMBER: 09/186,675

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 60/083,727

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/064,866

PRIOR FILING DATE: 1997-11-05

NUMBER OF SEQ ID NOS: 1558

SOFTWARE: PatentIn version 3.0

SEQ ID NO 64

LENGTH: 48

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: February 9, 2003, 17:18:47 : Search time 2362 Seconds
(without alignments)
11238.104 Million cell updates/sec

Title: US-09-960-143-3
Perfect score: 1639
Sequence: 1 acaaaacttcagacagca.....ataataattgttcaaaagt 1639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.8	1.5	43	17 AZ404728	AZ404728 IM0173108
2	23.2	1.4	46	13 BJ015738	BJ015738 BJ015738
C 3	23	1.4	50	12 BF029726	BF029726 601556615
C 4	22.8	1.4	46	14 BQ704909	BQ704909 Bn01_01c2
5	22.8	1.4	49	13 BJ054665	BJ054665 BJ054665
C 6	22.8	1.4	49	17 AZ333209	AZ333209 IM0062L10

7	22.6	1.4	46	9 AU009443	AU009443 AU009443
8	22.6	1.4	46	9 AU009444	AU009444 AU009444
9	22.4	1.4	48	9 AU266602	AU266602 AU266602
10	22.4	1.4	48	17 TA26E090	AL452944 T. brucei
C 11	22.4	1.4	49	17 AZ346760	AZ346760 IM0082F12
12	22.4	1.4	50	10 AZ333744	AW333744 S25E9 AGS
13	22.2	1.4	40	17 AZ615013	AZ615013 IM0444C09
14	22.2	1.4	48	13 BJ078372	BJ078372 BJ078372
15	22	1.3	50	9 AU268417	AU268417 AU268417
16	21.6	1.3	49	12 BG179823	BG179823 602332028
C 17	21.6	1.3	49	13 BI745472	BI745472 r81a10.Y
C 18	21.6	1.3	50	10 AV957350	AV957350 AV957350
19	21.4	1.3	44	17 BH853222	BH853222 SALK_0762
20	21.4	1.3	45	17 BH850240	BH850240 SALK_0710
21	21.2	1.3	47	17 TA48H05P	TA48H05P T. brucei
22	21.2	1.3	34	13 BJ052720	BJ052720 T. brucei
23	21.2	1.3	43	17 AZ586882	AZ586882 IM0394F11
24	21.2	1.3	45	9 AU267061	AU267061 AU267061
25	21.2	1.3	45	17 BH789466	BH789466 SALK_0296
26	21.2	1.3	45	17 BH799966	BH799966 1008110H1
C 27	21.2	1.3	45	17 TA344F02P	AL493895 T. brucei
C 28	21.2	1.3	50	17 BH861292	BH861292 SALK_0679
C 29	21.2	1.3	50	17 TA187C12P	AL477525 T. brucei
30	21	1.3	39	9 AU267631	AU267631 AU267631
C 31	21	1.3	43	14 T25548	T25548 EST00581 Un
32	21	1.3	47	9 AU265820	AU265820 AU265820
33	21	1.3	48	13 BJ083775	BJ083775 BJ083775
34	21	1.3	50	9 AU006647	AU006647 AU006647
35	21	1.3	50	17 AZ950287	AZ950287 2M0214K17
C 36	20.8	1.3	39	9 AU266450	AU266450 AU266450
C 37	20.8	1.3	44	10 AV834222	AV834222 AV834222
C 38	20.8	1.3	45	14 D34826	D34826 CELK013AYF
C 39	20.8	1.3	48	9 AU263470	AU263470 AU263470
C 40	20.8	1.3	48	12 BG667239	BG667239 DRABDB04
C 41	20.8	1.3	48	14 C21451	C21451 HUMGS001043
C 42	20.8	1.3	49	13 BI863578	BI863578 kx45h10.Y
C 43	20.6	1.3	45	17 BH792269	BH792269 SALK_0632
C 44	20.6	1.3	49	13 BI863578	BI863578 kx45h10.Y
45	20.6	1.3	50	13 BM126011	BM126011 IF04C10.X

ALIGNMENTS

RESULT 1
AZ404728
LOCUS IM0173108F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0173108 F, DNA sequence.
ACCESSION AZ404728
VERSION AZ404728.1 GI:10528741
KEYWORDS GSS.
SOURCE Mouse whole genome scaffolding with paired end reads from 10kb
ORGANISM house mouse.
MUS musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Y.

Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1..49
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL044pl3"
/clone_lib="NIBB Mochii normalized Xenopus neurula library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."

BASE COUNT 21 a 4 c 9 g 14 t 1 others
ORIGIN
Query Match 1.4%; Score 22.8; DB 13; Length 49;
Best Local Similarity 69.8%; Pred. No. 3.1e+06;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1580 GATTGTATGGAATAAAGTAAGAATATGAAACATTTAAAATA 1622
|| || || || || || || || || || || || || || || || || || ||
Db 6 GAGGGTCTTTAAAAATAAAGTCATTATCTAACAGTTAATA 48

RESULT 6
AZ333209/c
LOCUS AZ333209 49 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0062L10F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0062L10 F, DNA sequence.
ACCESSION AZ333209
VERSION AZ333209.1 GI:10397601
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT, 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: L column: 10
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 49.
Location/Qualifiers
1..49
/organism="Mus musculus"
/strain="C57BL/6J"

FEATURES
source
1..49
/organism="Mus musculus"
/strain="C57BL/6J"

TITLE
JOURNAL
COMMENT

Y.

Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1..49
/organism="Xenopus laevis"
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/clone="XL044pl3"
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/dev_stage="stage 15"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."

BASE COUNT 21 a 4 c 9 g 14 t 1 others
ORIGIN
Query Match 1.4%; Score 22.8; DB 13; Length 49;
Best Local Similarity 69.8%; Pred. No. 3.1e+06;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1580 GATTGTATGGAATAAAGTAAGAATATGAAACATTTAAAATA 1622
|| || || || || || || || || || || || || || || || || || ||
Db 6 GAGGGTCTTTAAAAATAAAGTCATTATCTAACAGTTAATA 48

RESULT 6
AZ333209/c
LOCUS AZ333209 49 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0062L10F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0062L10 F, DNA sequence.
ACCESSION AZ333209
VERSION AZ333209.1 GI:10397601
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT, 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: L column: 10
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 49.
Location/Qualifiers
1..49
/organism="Mus musculus"
/strain="C57BL/6J"

FEATURES
source
1..49
/organism="Mus musculus"
/strain="C57BL/6J"

TITLE
JOURNAL
COMMENT

Y.

Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1..49
/organism="Xenopus laevis"
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/tissue_type="whole embryo"
/dev_stage="stage 15"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."

BASE COUNT 21 a 4 c 9 g 14 t 1 others
ORIGIN
Query Match 1.4%; Score 22.8; DB 13; Length 49;
Best Local Similarity 69.8%; Pred. No. 3.1e+06;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1580 GATTGTATGGAATAAAGTAAGAATATGAAACATTTAAAATA 1622
|| || || || || || || || || || || || || || || || || || ||
Db 6 GAGGGTCTTTAAAAATAAAGTCATTATCTAACAGTTAATA 48

RESULT 6
AZ333209/c
LOCUS AZ333209 49 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0062L10F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0062L10 F, DNA sequence.
ACCESSION AZ333209
VERSION AZ333209.1 GI:10397601
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT, 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: L column: 10
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 49.
Location/Qualifiers
1..49
/organism="Mus musculus"
/strain="C57BL/6J"

FEATURES
source
1..49
/organism="Mus musculus"
/strain="C57BL/6J"

TITLE
JOURNAL
COMMENT

Y.

Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1..49
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL044pl3"
/clone_lib="NIBB Mochii normalized Xenopus neurula library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."

BASE COUNT 21 a 4 c 9 g 14 t 1 others
ORIGIN
Query Match 1.4%; Score 22.8; DB 13; Length 49;
Best Local Similarity 69.8%; Pred. No. 3.1e+06;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1580 GATTGTATGGAATAAAGTAAGAATATGAAACATTTAAAATA 1622
|| || || || || || || || || || || || || || || || || || ||
Db 6 GAGGGTCTTTAAAAATAAAGTCATTATCTAACAGTTAATA 48

RESULT 6
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/db_xref="taxon:10090"
/clone="UUGC1M062L10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 (g147321141gb/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      24 a      0 c      0 g      25 t
ORIGIN
Query Match      1.4%; Score 22.8; DB 17; Length 49;
Best Local Similarity 71.4%; Pred. No. 3.1e+06;
Matches 30; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1139 TAAATTTATTTATTTAGATATTAATGATGTTTATTAGA 1180
      III I IIII III I IIII III I I IIII I
DB 43 TAATTATATATATATATATATATATATATATATATATA 2

RESULT 7
AU009443
LOCUS      46 bp mRNA linear EST 31-JUL-1998
DEFINITION Schizosaccharomyces pombe cdna clone spc04922, mRNA sequence.
ACCESSION AU009443
VERSION AU009443.1 GI:3346123
KEYWORDS EST.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
          Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
          Schizosaccharomycetales; Schizosaccharomycetaceae;
          Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 46)
AUTHORS Morimyo,M. and Mita,K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe

FEATURES
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        /clone="spc04922"
        /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
        /sex="h minus"
        /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT      27 a      2 c      3 g      14 t
ORIGIN
Query Match      1.4%; Score 22.6; DB 9; Length 46;
Best Local Similarity 68.9%; Pred. No. 3.4e+06;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 582 ATACTTATATGTAAGACTATTTATTTTGAATCTACAAAAACAA 626
      I I IIII IIII I I IIII III I IIII III
DB 2 AAAATTATACTTTAAATAATTAATTAATTTGAATTTGACAAAAAANA 46

RESULT 8
AU009444
LOCUS      46 bp mRNA linear EST 31-JUL-1998
DEFINITION Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU009444
VERSION AU009444.1 GI:3346124
KEYWORDS EST.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
          Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
          Schizosaccharomycetales; Schizosaccharomycetaceae;
          Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 46)
AUTHORS Morimyo,M. and Mita,K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe

FEATURES
    source
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        /organism="Schizosaccharomyces pombe"
        /strain="972"
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        /clone="spc04923"
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        /sex="h minus"
        /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT      27 a      2 c      3 g      14 t
ORIGIN
Query Match      1.4%; Score 22.6; DB 9; Length 46;
Best Local Similarity 68.9%; Pred. No. 3.4e+06;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 582 ATACTTATATGTAAGACTATTTATTTTGAATCTACAAAAACAA 626
      I I IIII IIII I I IIII III I IIII III
DB 2 AAAATTATACTTTAAATAATTAATTAATTTGAATTTGACAAAAAANA 46

RESULT 9
AU266602
LOCUS      48 bp mRNA linear EST 10-MAY-2002
DEFINITION VS Dictyostellium discoidium cDNA clone VSG534 5', mRNA
ACCESSION AU266602
VERSION AU266602.1 GI:20525400
KEYWORDS EST.
SOURCE Dictyostellium discoidium.
ORGANISM Dictyostellium discoidium
          Eukaryota; Mycetozoa; Dictyostelidia; Dictyostellium.
REFERENCE 1 (bases 1 to 48)

```

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AUTHORS      Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
              Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE        Population analysis of cDNAs from unicellular and multicellular
              stages of Dictyostelium discoideum
JOURNAL      Unpublished (2002)
COMMENT      Contact: Hideko Urushihara
              Institute of Biological Sciences
              University of Tsukuba
              1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
              Tel: 81-298-53-4664
              Fax: 81-298-53-6614
              Email: hideko@biol.tsukuba.ac.jp.

FEATURES     source
              1. .48
              Location/Qualifiers
                /organism="Dictyostelium discoideum"
                /strain="AX4"
                /db_xref="taxon:44689"
                /clone="VSG534"
                /clone_lib="VS"
                /sex="mat A"
                /dev_stage="vegetative"
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BASE COUNT   30 a      3 c      1 g      14 t
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Query Match      1.4%; Score 22.4; DB 9; Length 48;
Best Local Similarity 66.7%; Pred. No. 3.6e+06;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy  576 CAGACATACCTATATGTAAGTATTTATTTATTTGAATCTACAAAAA 623
      1 111 11 111 1111 1111 111 111 11111
Db  1 CCGAAAAACAATATAATATAATTTTATTTTATATAAAAAAAA 48

RESULT 10
TA26E09Q LOCUS      48 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 26e09, reverse sequence,
            genomic survey sequence.
ACCESSION  AL452944
VERSION    AL452944.1 GI:11850929
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
            Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
            1 (bases 1 to 48)
REFERENCE  Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
            Direct Submission
            Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
            Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T-brucei/.
            Location/Qualifiers
              1. .48
              /organism="Trypanosoma brucei"
              /strain="TREU927"
              /db_xref="taxon:5691"
              /clone="26e09"
            18 a      7 c      8 g      15 t

BASE COUNT   18 a      7 c      8 g      15 t

ORIGIN
Query Match      1.4%; Score 22.4; DB 17; Length 48;
Best Local Similarity 72.5%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy  1485 ATATTATTTAAATGACTGCATTTTAAATACAAGGCTTTA 1524
      11111 111 1111 1111111111 111
Db  7 ATATTATTAACAGTGTGCACATTAATAACAAGTGCTA 46

RESULT 11
AZ346760/c LOCUS      49 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION IM0082F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0082F12 F, DNA sequence.
ACCESSION  AZ346760
VERSION    AZ346760.1 GI:10425997
KEYWORDS   GSS.
SOURCE     house mouse.
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
            1 (bases 1 to 49)
REFERENCE  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT.
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0082 row: F column: 12
            Seq primer: CGTTGTAACGACGCGCAGT
            Class: plasmid ends
            High quality sequence stop: 49.
            Location/Qualifiers
              1. .49
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              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC1M0082F12"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
              /note="vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptored DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gil4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptored mouse DNA was annealed to
            adaptored vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
            39 a      4 c      0 g      6 t

BASE COUNT   39 a      4 c      0 g      6 t

```

ORIGIN

Query Match 1.4%; Score 22.4; DB 17; Length 49;
Best Local Similarity 66.7%; Pred. No. 3.6e+06;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1014 ATTTCAAGTGAACCTATTATTAACCTATTATTATTATTATTATTATTATT 1061
Db 49 ATTGTTTCTTTGTTTATTATTATTATTATTATTATTATTATTATTGTTT 2

RESULT 12
AW333744
LOCUS
DEFINITION S25E9 AGS-1 Pneumocystis carinii f. sp. carinii CDNA 3', mRNA
sequence.
ACCESSION AW333744
VERSION AW333744.1 GI:6830101
KEYWORDS EST.
SOURCE
ORGANISM

Pneumocystis carinii f. sp. carinii.
Pneumocystis carinii f. sp. carinii.
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.

REFERENCE
1 (bases 1 to 50)
AUTHORS Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Edman
,J.C., Kovacs,J. and Cushion,M.
, J.C., Kovacs,J. and Cushion,M.
' TITLE
JOURNAL Expressed sequence tags from Pneumocystis carinii
COMMENT Unpublished (2000)
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES
source
1..50
Location/Qualifiers
/organism="Pneumocystis carinii f. sp. carinii"
/db_xref="taxon:38081"
/clone_lib="AGS-1"
/lab_host="E. coli"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

BASE COUNT 21 a 1 c 1 g 27 t

Query Match 1.4%; Score 22.4; DB 10; Length 50;
Best Local Similarity 66.7%; Pred. No. 3.6e+06;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1143 TTTATTATTTTATAGATTAATGAAGCTTTTATTAGATAAATTCAA 1190
Db 2 TTTTATTTTATTTTAAAAAATGAAAAATATAAATCTATTAAA 49

RESULT 13
AZ615013
LOCUS
DEFINITION M0444C09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0444C09 F, DNA sequence.
ACCESSION AZ615013
VERSION AZ615013.1 GI:11737203
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 40)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddu@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0444 row: C column: 09
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 40.

TITLE
JOURNAL
COMMENT

FEATURES
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1..40
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0444C09"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (gil4732114[gb]AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 13 a 0 c 1 g 26 t

Query Match 1.4%; Score 22.2; DB 17; Length 40;
Best Local Similarity 77.1%; Pred. No. 4.1e+06;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1044 TTATTATGTTTATTATTAAGCATCAATATTCT 1078
Db 3 TTATTATTTATTATTATTATTATTATTATTATCT 37

RESULT 14
BJ078372
LOCUS
DEFINITION BJ078372 NIBB Mochii normalized xenopus tailbud library Xenopus
laevis cDNA clone XL063p03 3', mRNA sequence.
ACCESSION BJ078372
VERSION BJ078372.1 GI:17523288
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.

REFERENCE	1. (bases 1 to 48)
AUTHORS	Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.
TITLE	Expressed genes in <i>X. laevis</i> embryo
JOURNAL	Unpublished (2001)
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetiscs 1111 Yata, Mashima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.

```

FEATURES
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    1. .48
      Location/Qualifiers
        /organism="Xenopus laevis"
        /db_xref="taxon:8355"
        /clone="Xl063p03"
        /clone_lib="NIBB Wochli normalized xenopus tailbud
        library"

```

```
library
/tissue_type="whole embryo"
/dev_stage="stage 25"
/note="vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
24 a 6 c 5 g 13 t
BASE COUNT
```

Query Match	1.4%	Score 22.2;	DB 13;	Length 48;
Best Local Similarity	77.1%;	Pred. No. 3.9e+05;		
Matches 27; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	602	ATTTATTGAACTCTACAAAAAACACAAAATAATTT	636
Db	14	ATGGACTTGAATTTAAAAAAAATAAAAAATAATCT	48

RESULT 15	LOCUS	DEFINITION	50 bp	mRNA	linear	EST 10-MAY-2002
AU268417	AU268417	AU268417 VS Dictyostelium discoideum cDNA clone VSI266 5', mRNA sequence.				

ACCESSION AU268417
 VERSION AU268417.1 GI:20527215
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum.
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 REFERENCE 1 (bases 1 to 50)

REFERENCE	1 (pages 1 to 30)
AUTHORS	Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.
TITLE	Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL	Unpublished (2002)
COMMENT	Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan Tel: 81-298-53-4664 Fax: 81-298-53-6614 Email: hidekoebi@tsukuba.ac.jp.

```

FEATURES
  source
    1. .50
      /organism="Dictyostelium discoideum"
      /strain="AX4"
      /db_xref="taxon:44689"
      /clone="VSI266"
      /clone_lib="VS"
      /sex="mat A"
      /dev_stage="proctative"

```

	BASE COUNT	ORIGIN	/dev_stage=	vegetative
	30 a	1 c	3 g	16 t

Query Match . 1.3%; Score 22; DB 9; Length 50;
Best Local Similarity 67.4%; Pred. No. 4.2e+06;
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 578 GAACATACITATATGTAAGTATTATTATTGAATCTACAAAAA 623

Db 5 GAAAAACCAATATAATATAATTTTATTTTATATAAAAAA 50

RESULT 16	
BG179823	
LOCUS	BG179823
DEFINITION	602329028F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4430262 5', mRNA sequence.
	49 bp mRNA linear EST 06-FEB-2001

mRNA sequence.
 ACCESSION BG179823
 VERSION BG179823.1 GI:12686526
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/PTP

Issue: Procurement: DCID/DIR.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: WGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM10183 row: h column: 07
 High quality sequence stop: 49.

FEATURES	SOURCE
1. <i>General</i>	
2. <i>Specific</i>	
3. <i>Other</i>	
4. <i>Other</i>	
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100. <i>Other</i>	

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:443062"
/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-res
/notes="Organ: prostate; Vec
Site.2: SalI; Cloned undir
Average insert size 1.4 Kb.
full-length clones and cons
Note: This is a NIH_MGC lib
32 a 4 c 4 q 9 t
BASE COUNT

```

BASE COUNT 32 a 4 c 4 g 9 t

ORIGIN

NOTE: THIS IS A NIH-MSC LIBRARY.

Query Match 1.3%; Score 21.6; DB 12; Length 49;
Best Local Similarity 68.2%; Pred. NO. 5e+06;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1177 TAGATAAAATTTCATCAAGGGTTTTTAGATTAAACAACAAACAA 1220
|| ||||||| || ||||| | ||||| ||||| ||||| ||
Dd 5 TATATAAATAAAAACAAGGCTTTTGGAAAAATAAAAAAAAAAAAAA 48

RESULT 17	
BI745472/c	
LOCUS	BI745472 49 bp mRNA linear EST 25-SEP-2001
DEFINITION	rk8la10.y3 Meloidogyne javanica egg pamp1 v6 Chiapelli McCarter
	Meloidogyne javanica cDNA 5', mRNA sequence.
ACCESSION	BI745472
VERSION	BI745472.1
KEYWORDS	GI:15767274
SOURCE	EST.
	root-knot nematode.
ORGANISM	Meloidogyne javanica
	Eukaryota; Metazoa; Nematoda;
	Chromadorea; Tylenchida
	Tylenchina;

Search completed: February 9, 2003, 19:20:11
Job time : 2368 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: February 9, 2003, 15:17:21 ; Search time 340 seconds
(without alignments)
10855.957 Million cell updates/sec

Title: US-09-960-143-3
Perfect score: 1639
Sequence: 1 acaaaccttcagacagca.....atataattgttcgaagt 1639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*

24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	2.3	37	18 AAT76272	Human MDNCF antise
2	37	2.3	37	20 AAX54069	Monocyte-derived n
3	37	2.3	37	21 AAF19635	Human monocyte der
4	37	2.3	37	21 AAA33513	Low adenosine anti
5	34	2.1	34	18 AAT76366	Human interleukin
6	34	2.1	34	20 AAX54167	Human IL-8 antisen
7	34	2.1	34	21 AAF19733	Human interleukin-
8	34	2.1	34	21 AAA33611	Low adenosine anti
9	33	2.0	33	14 AAQ37164	Anti-sense primer

C 10	33	2.0	33	17 AAT38979	Interleukin IL-8 3
C 11	33	2.0	33	20 AAV65360	Interleukin-8 anti
C 12	33	2.0	33	20 AAV08015	Primer IL-8 for In
C 13	31	1.9	31	18 AAT45913	Human interleukin-
C 14	31	1.9	31	22 AAI30870	Human single nucle
C 15	30	1.8	30	17 AAT45757	Human interleukin-
C 16	30	1.8	30	19 AAV61828	PCR primer for hum
C 17	30	1.8	30	19 AAV35562	Human interleukin
C 18	30	1.8	30	19 AAV35781	PCR primer IL8p2 o
C 19	30	1.8	30	22 AAC88174	Human interleukin-
C 20	30	1.8	30	24 ABL46338	Human interleukin-
C 21	29	1.8	30	19 AAV24558	IL-8 antisense oli
C 22	28	1.7	28	24 ABK66391	Human gene specifi
C 23	28	1.7	28	24 ABK66392	Human gene specifi
C 24	26	1.6	26	24 AAD21908	PCR primer, 2767T
C 25	25.2	1.5	39	18 AAT61103	Chimeric chemokine
C 26	25.2	1.5	39	18 AAT61104	Chimeric chemokine
C 27	25	1.5	25	17 AAT29243	Human interleukin-
C 28	25	1.5	25	18 AAT45912	Human interleukin-
C 29	25	1.5	25	21 AAA65326	B-thromboglobulin
C 30	25	1.5	25	24 AAD39024	Human beta-actin s
C 31	25	1.5	25	24 AAD37345	Interleukin-8 (IL-
C 32	25	1.5	25	24 ABK14346	Human interleukin-
C 33	25	1.5	26	24 AAD21907	Human interleukin-
C 34	24.4	1.5	48	18 AAT61099	Chimeric chemokine
C 35	24	1.5	24	18 AAT45911	Human interleukin-
C 36	24	1.5	24	24 AAD39023	Human beta-actin s
C 37	24	1.5	24	24 AAD37344	Interleukin-8 (IL-
C 38	24	1.5	48	22 AAH30030	Human interleukin
C 39	23.6	1.4	39	18 AAT61109	Chimeric chemokine
C 40	23.6	1.4	39	18 AAT61110	Chimeric chemokine
C 41	23	1.4	23	17 AAT29242	Human interleukin-
C 42	23	1.4	23	18 AAT76365	Human interleukin
C 43	23	1.4	23	20 AAX54166	Human IL-8 antisen
C 44	23	1.4	23	21 AAF19732	Human interleukin-
C 45	23	1.4	23	21 AAA33610	Low adenosine anti

ALIGNMENTS

RESULT 1
AAT76272/C
ID AAT76272 standard; DNA; 37 BP.
XX
XX
XX AAT76272;

DT 15-SEP-1997 (first entry)
XX Human MDNCF antisease oligonucleotide HSMDCNFAS2.
DE
XX
XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis;
KW monocyte-derived neutrophil chemotactic factor; ss.
XX
OS Synthetic.
XX
XX WO9640162-A1.
XX
PD 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US09306.
XX
XX 07-JUN-1995; 95US-0474497.
PR (UYEC-) UNIV EAST CAROLINA.
XX
XX Metzger WJ, Nyce JW;
XX
XX WPI; 1997-051871/05.
XX
XX Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of

PT subject
XX Claim 5; Page 33; 71pp; English.
PS
XX
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC HSMNCFAS2 specific for the human monocyte-derived neutrophil
CC chemotactic factor. The method can be used to treat airway diseases
CC such as cystic fibrosis, asthma, chronic obstructive pulmonary disease,
CC bronchitis and other airway diseases characterised by an inflammatory
CC response. By eliminating adenosine from the antisense ON, its
CC liberation upon antisense degradation is prevented, thereby preventing
CC adenosine-induced bronchoconstriction in patients with hyper-reactive
CC airways.
XX
SQ Sequence 37 BP; 0 A; 11 C; 9 G; 17 T; 0 other;

Query Match 2.3%; Score 37; DB 18; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AGGACAAGAGCCAGGAGGAAGAACCCGCGGAGGAACCA 73
DB 37 AGGACAAGAGCCAGGAGGAAGAACCCGCGGAGGAACCA 1
|||||
RESULT 2
AA54069/c
ID AAX54069 standard; DNA; 37 BP.
XX
AC AAX54069;
XX
DT 05-JUL-1999 (first entry)
XX
DE Monocyte-derived neutrophil chemotactic factor antisense oligo.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US19419.
XX
PR 09-JUN-1998; 98US-0093972.
XX
PR 17-SEP-1997; 97US-0059160.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
PI
DR WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction
PT
XX Disclosure; Page 51; 120pp; English.
PS
XX The specification describes antisense oligonucleotides (AAX52869-X55271)
XX directed against at least 2 mRNAs selected from target genes, coding and
CC

CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences AAX55272-74. These multiple target
CC oligonucleotides (specifically AAX55180-271) can be used for the
CC antisense treatment of diseases and conditions. Typical diseases and
CC conditions are those associated with impaired respiration and
CC inflammation, including lung diseases, pulmonary vasoconstriction,
CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC hepatic metastases, as well as all types of cancers which may metastasize
CC or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ Sequence 37 BP; 0 A; 11 C; 9 G; 17 T; 0 other;

Query Match 2.3%; Score 37; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AGGACAAGAGCCAGGAGGAAGAACCCGCGGAGGAACCA 73
DB 37 AGGACAAGAGCCAGGAGGAAGAACCCGCGGAGGAACCA 1
|||||
RESULT 3
AAF19635/G
ID AAF19635 standard; DNA; 37 BP.
XX
AC AAF19635;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human monocyte derived neutrophil chemotactic factor DNA fragment #1202.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX (NYCE/) NYCE J W.
XX
XX Nyce JW;
PI
DR WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
XX trigger adenosine receptors during metabolism, useful e.g. for treating
XX cancers and respiratory obstructions -
PS Claim 14; Page 210; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.

XX SQ Sequence 37 BP; 0 A; 11 C; 9 G; 17 T; 0 other;

Query Match 2.3%; Score 37; DB 21; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 AGGACAAGAGCCAGGAGAAACCCGGAAGGAACCA 73
Db 37 AGGACAAGAGCCAGGAGAAACCCGGAAGGAACCA 1

RESULT 4
AAA33513/C
ID: AAA33513 standard; DNA; 37 BP.

XX AAA33513;

XX 28-JUL-2000 (first entry)

XX Low adenosine antisense oligonucleotide SEQ ID NO:1202.

XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

XX

PI Nyce JW;
XX WPI; 2000-205971/18.
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Claim 18; Page 415; 1343pp; English.

XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 1%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX SQ Sequence 37 BP; 0 A; 11 C; 9 G; 17 T; 0 other;

Query Match 2.3%; Score 37; DB 21; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 AGGACAAGAGCCAGGAGAAACCCGGAAGGAACCA 73
Db 37 AGGACAAGAGCCAGGAGAAACCCGGAAGGAACCA 1

RESULT 5
AAT76366/C

XX AAT76366 standard; DNA; 34 BP.

XX AAT76366;

XX 15-SEP-1997 (first entry)

XX Human interleukin 8 antisense oligonucleotide HUMTL8AAS3.

XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.

XX Synthetic.

XX WO9640162-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US09306.

XX 07-JUN-1995; 95US-0474497.

XX (UYEC-) UNIV EAST CAROLINA.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 XX Claim 14; Page 236; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.

XX Sequence 34 BP; 0 A; 11 C; 7 G; 16 T; 0 other;

Query Match 2.1%; Score 34; DB 21; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 37 AGGACAAGAGCCAGGAGAAACCCCGGAAGGAA 70
 Db 34 AGGACAAGAGCCAGGAGAAACCCCGGAAGGAA 1

RESULT 8
 AAA33611/c
 ID AAA33611 standard; DNA; 34 BP.

XX AC AAA33611;

XX 28-JUL-2000 (first entry)

DE Low adenosine antisense oligonucleotide SEQ ID NO:1300.

XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.
 PR (UYEC-) UNIV EAST CAROLINA.
 XX Nyce JW;
 PI WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 CC vasoconstriction, inflammation, allergies, asthma, hypertension,
 CC bronchitis, emphysema, respiratory distress syndrome, ischemia or
 CC cancers -
 PS Claim 18; Page 427; 1343pp; English.

XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiasthmatic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.

XX Sequence 34 BP; 0 A; 11 C; 7 G; 16 T; 0 other;

Query Match 2.1%; Score 34; DB 21; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 37 AGGACAAGAGCCAGGAGAAACCCCGGAAGGAA 70
 Db 34 AGGACAAGAGCCAGGAGAAACCCCGGAAGGAA 1

RESULT 9
 AAA337164/c
 ID AAA337164 standard; DNA; 33 BP.

XX AC AAA337164;

XX 23-JUN-1993 (first entry)

XX Anti-sense primer to amplify IL-8.

XX Interleukin-8; polymerase chain reaction; PCR;
 KW cytokine synthesis inhibitor; inflammation;
 KW monokine production; Southern analysis; ss.

XX Synthetic.

XX WO9302693-A.

XX 18-FEB-1993.

PF 06-AUG-1992; 92WO-US06378.
 XX
 PR 06-AUG-1991; 91US-0742129.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI De Waal Malefyt R, Howard M, Hsu DH, Ishida H, OGarra A;
 PI Spits H, Zlotnik A;
 XX
 DR WPI; 1993-076172/09.
 XX
 XX Use of interleukin-10 to modulate inflammation or T-cell mediated
 PT immune function - for treating septic and toxic shock,
 PT auto-immune diseases, tumours and infectious diseases
 XX
 PS Example B6; Page 87; 208pp; English.
 XX
 CC To determine at which level IL-10 inhibited the production of
 CC cytokines by monocytes, comparative PCR analyses were performed on
 CC RNA isolated from monocytes, activated by LPS in the presence or
 CC absence of IL-10, IL-4 or the neutralising anti-IL-10 MAb for 24
 CC hours. mRNA isolated from the samples was reverse transcribed into
 CC cDNA and amplified by cytokine-specific primers. Primer AAQ37164 is
 CC specific to IL-8 (see AAQ37163 for sense primer). It was
 CC found that IL-1 alpha, IL-6, TNF alpha, GM-CSF and G-CSF expression
 CC was strongly inhibited by IL-10 and IL-4 at the mRNA level. IL-1 beta
 CC and IL-8 expression was only slightly affected by IL-10.
 XX
 SQ Sequence 33 BP; 9 A; 10 C; 2 G; 12 T; 0 other;
 Query Match 2.0%; Score 33; DB 14; Length 33;
 - Best Local Similarity 100.0%; Pred. No. 6.5e+03;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 358 GAGAAGTTTTCAGAGGGCTGAGAAATTCATAA 390
 DB 33 GAGAAGTTTTCAGAGGGCTGAGAAATTCATAA 1
 RESULT 10
 AAT38979/c
 ID AAT38979 standard; DNA; 33 BP.
 XX
 AC AAT38979;
 XX
 DT 29-MAY-1997 (first entry)
 XX
 DE Interleukin IL-8 3' PCR primer.
 XX
 KW Cytokine; expression profile; genital wart; interleukin 12; IL-12;
 KW tumour regression; adjuvant; polymerase chain reaction; PCR;
 KW condyloma acuminata; human papilloma virus; HPV-6; HPV-11; HPV16;
 KW HPV18; anogenital; cutaneous; laryngeal; oesophageal; cancer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9629091-A1.
 XX
 PD 26-SEP-1996.
 XX
 PF 22-MAR-1996; 96WO-GB00686.
 XX
 PR 22-MAR-1995; 95GB-0005784.
 XX
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 PI Scarpini CG, Stanley MA;
 XX
 DR WPI; 1996-442947/44.
 XX
 PT Use of interleukin-12 to treat papilloma virus-associated lesions -
 PT esp. as a vaccine adjuvant with papilloma virus antigen for
 PT immuno:therapy of warts or tumours

XX
 PS Disclosure; Page 14; 32pp; English.
 XX
 CC RNA was extracted from genital lesions, reverse transcribed to
 CC produce cDNA and then the cDNA was used as the template for PCR
 CC amplification of various cytokines using the primers in AAT38964-
 CC AAT39005. To confirm the identity of amplified cDNA, digoxigenin-
 CC labelled probes specific for each cytokine (see AAT39006-T39021)
 CC were hybridised with Southern blots of amplified sequences. The
 CC expression profile for regressing and non-regressing warts was
 CC established and compared to cytokine expression patterns in normal
 CC cervical tissue. Results showed that interleukin 12 is barely
 CC expressed (if at all) in non-regressing warts, but is expressed in
 CC regressing warts. This suggests a central role for IL-12 in wart
 CC regression. It has been found that IL-12 can be used (especially
 CC as a vaccine adjuvant) for treating papilloma virus-associated
 CC lesions such as condyloma acuminata (anogenital warts) caused by
 CC human papilloma virus type 6 (HPV-6) and/or HPV-11 and more
 CC generally for treatment of tumours associated with HPV16 and HPV18
 CC infection e.g. anogenital, cutaneous, laryngeal and oesophageal
 CC cancers.
 XX
 SQ Sequence 33 BP; 9 A; 10 C; 2 G; 12 T; 0 other;
 Query Match 2.0%; Score 33; DB 17; Length 33;
 - Best Local Similarity 100.0%; Pred. No. 6.5e+03;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 358 GAGAAGTTTTCAGAGGGCTGAGAAATTCATAA 390
 DB 33 GAGAAGTTTTCAGAGGGCTGAGAAATTCATAA 1
 RESULT 11
 AAV65360/c
 ID AAV65360 standard; DNA; 33 BP.
 XX
 AC AAV65360;
 XX
 DT 22-JAN-1999 (first entry)
 XX
 DE Interleukin-8 antisense primer.
 XX
 KW Interleukin; IL-10; IL-6; IL-8; inflammatory response; endotoxin;
 KW tumour necrosis factor alpha; TNF; IL-1 alpha; IL-1 beta; bacteria;
 KW septic; toxic shock; superantigen; T-cell dependent response; human;
 KW viral; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5837293-A.
 XX
 PD 17-NOV-1998.
 XX
 PF 07-JUN-1995; 95US-0481560.
 XX
 PR 24-MAR-1995; 95US-0410654.
 PR 06-AUG-1991; 91US-0742129.
 PR 06-AUG-1992; 92US-0926853.
 PR 19-APR-1994; 94US-0229854.
 PR 07-JUN-1995; 95US-0481560.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI De Waal Malefyt R, Howard M, Hsu D, Ishida H, O'Garra A;
 PI Spits H, Zlotnik A;
 XX
 DR WPI; 1999-023391/02.
 XX
 PT Reducing inflammatory response by treatment with interleukin-10 -
 PT particularly for treating bacterial infections, e.g. septic or toxic
 PT shock

XX Example 14; Column 42; 108pp; English.

PS Sequences AAV5353 to AAV6370 represent PCR primers used during the

XX course of the invention. The invention provides a method for reducing

CC inflammatory response characterised by elevated levels of interleukin

CC (IL)-1 alpha, IL-1 beta, IL-6 or IL-8, or of tumour necrosis factor

CC (TNF) alpha which comprises administering IL-10. The IL-10 to be

CC administered is a recombinant mature protein selected from the sequences

CC of human IL-10 (AAW81421, AAW81423) or viral IL-10 (AAW81422, AAW81423).

CC IL-10 is especially administered to humans at risk of developing an

CC inflammatory response, particularly where this is caused by infection by

CC gram-positive or negative bacteria that produce endotoxins. Specific

CC applications are in cases of septic or toxic shock and where infection

CC results in a T-cell dependent response. Treatment with IL-10 reduces

CC levels of the proinflammatory cytokines (by reducing their synthesis in

CC monocytes, macrophages and natural killer cells), and inhibits activation

CC of T cells by superantigens.

XX Sequence 33 BP; 9 A; 10 C; 2 G; 12 T; 0 other;

SQ Query Match 2.0%; Score 33; DB 20; Length 33;

Best Local Similarity 100.0%; Pred. No. 6.5e+03;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAGTTTTCGAGAGGGCTGAGAAATTCATAA 390

DB 33 GAGAGTTTTCGAGAGGGCTGAGAAATTCATAA 1

RESULT 12

AAV08015/C

ID AAV08015 standard; DNA; 33 BP.

XX AAV08015;

AC AAV08015;

DT 20-JAN-1999 (first entry)

XX- Primer IL-8 for Interleukin-10 coding sequence.

DE Interleukin-10; IL-10; septic shock; bacterial infection; toxic shock;

XX infectious shock; inflammation; immune response modulation; therapy;

KW PCR primer; ss.

XX Synthetic.

OS US5833976-A.

PN 10-NOV-1998.

XX 24-MAR-1995; 95US-0410654.

PF 06-AUG-1992; 92US-0926853.

XX 06-AUG-1991; 91US-0742129.

PR 19-APR-1994; 94US-0229854.

XX 24-MAR-1995; 95US-0410654.

XX (SCHE) SCHERING CORP.

PA De Waal Malefyt R, Howard M, Hsu D, Ishida H, O'Garra A;

XX Spits H, Zlotnik A;

PI WPI; 1999-008644/01.

DR Treating shock conditions from e.g. bacterial infections - comprises

XX administering interleukin-10

PT Example 14; Column 43; 109pp; English.

PS This sequence represents a primer for a interleukin-10 (IL-10) coding

XX sequence. The IL-10 protein can be used in the method of the invention

CC for ameliorating a symptom of: (a) septic shock in a host suffering from

CC a bacterial (preferably gram negative) infection; (b) toxic shock;

CC (c) infectious shock; or (d) inflammation. The method comprises

CC administering a biologically active IL-10 (preferably human) protein,

CC analogue or a fragment (preferably full length). The treatment is used to

CC modulate immune responses caused by the different shock syndromes, which

CC are endotoxin or superantigen induced toxicity, or autoimmune related

CC conditions. The conditions are side-effects of microbial infections,

CC caused by release of their protein products, especially on anti-microbial

CC treatment, which when cells are killed, they lyse, releasing proteins

CC which induce the shock conditions. IL-10 inhibits TNF-alpha (tumour

CC necrosis factor-alpha) and TNF-gamma synthesis, which as part of an

CC immune response elicits the shock syndromes.

XX Sequence 33 BP; 9 A; 10 C; 2 G; 12 T; 0 other;

SQ Query Match 2.0%; Score 33; DB 20; Length 33;

Best Local Similarity 100.0%; Pred. No. 6.5e+03;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAGTTTTCGAGAGGGCTGAGAAATTCATAA 390

DB 33 GAGAGTTTTCGAGAGGGCTGAGAAATTCATAA 1

RESULT 13

AAAT45913/C

ID AAT45913 standard; DNA; 31 BP.

XX AAT45913;

AC AAT45913;

DT 01-SEP-1997 (first entry)

XX Human interleukin-8 PCR product hybridisation probe.

DE Interleukin 8; IL-8; polymerase chain reaction; PCR primer;

XX detection; diagnosis; cytokine; renal transplant rejection;

KW immunoassay; detergent chaotrope; ss.

XX Synthetic.

OS Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /*note= "labelled with FITC"

XX WO9639536-A1.

XX 12-DEC-1996.

XX 31-MAY-1996; 96WO-US08142.

XX 06-JUN-1995; 95US-0467909.

XX (TCEL-) T CELL DIAGNOSTICS INC.

XX Emmett C, Foster KA;

XX WPI; 1997-043157/04.

XX Quantification of mRNA expression levels - using universal enzyme

XX linked immunosorbent assay, for rapid diagnosis of disease and

XX transplant rejection

XX Example 5; Page 10; 19pp; English.

XX A new method for the quantification of mRNA expression levels can

XX be used for detecting the cytokine interleukin-8. In the method,

XX total RNA is extracted from a sample, preferably using a detergent

XX chaotrope lysis mixture, and cDNA is synthesised from mRNA. This

XX cDNA is added to nucleotides, Taq polymerase, a magnesium source,

XX a 3'-primer and a 5'-primer labelled with a molecule capable of

XX binding to a coated microtitre plate and a PCR reaction is performed.

XX A probe, capable of hybridising to the PCR product and labelled with

XX a detectable marker or containing a molecule capable of binding to

CC an agent coated on a microtitre plate is added to the PCR product. A
 CC mixture of hybridised probe and PCR product, unhybridised probe and
 CC PCR products and excess primers are transferred to a microtitre plate
 CC coated with an agent capable of binding to a molecule on the PCR
 CC product, or the molecule on the probe. The detectable marker is
 CC detected on a bound hybridised probe and PCR product, preferably
 CC via the detection of an antibody that detects the labelled primer
 CC or probe, so that mRNA levels can be determined. primer and probe
 CC sequences which can be used for the detection of interleukin-8
 CC include the present sequence.

XX
 SQ Sequence 31 BP; 11 A; 8 C; 9 G; 3 T; 0 other;
 Query Match 1.9%; Score 31; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 TGGCAGCCTTCTGATTTCTGCAGCTCTGTG 149
 |||||
 Db 31 TGGCAGCCTTCTGATTTCTGCAGCTCTGTG 1

RESULT 14
 AAI30870
 ID AAI30870 standard; DNA; 31 BP.
 AC AAI30870;
 XX
 XX 18-OCT-2001 (first entry)
 DT
 DE Human single nucleotide polymorphism (SNP) IL8.
 XX-
 KW Human; resequence; genotype; disease; forensic; paternity testing;
 KW single nucleotide polymorphism; SNP; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT replace(16.C)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO20016680-A2.
 PD 13-SEP-2001.
 XX
 XX 07-MAR-2001; 2001WO-US07268.
 XX
 PR 07-MAR-2000; 2000US-0187510.
 PR 22-MAY-2000; 2000US-0206129.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2001-522952/57.
 XX
 XX Nucleic acid molecules from the human genome which include polymorphic
 PT sites, useful in methods for predicting the presence, absence or
 PT severity of a particular phenotype or disorder (e.g. diabetes)
 PT associated with a particular genotype -
 XX
 PS Claim 1; Page 113; 145pp; English.
 CC
 CC The invention relates to the identification of nucleic acid molecules
 CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
 CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing.

XX
 SQ Sequence 31 BP; 12 A; 8 C; 4 G; 7 T; 0 other;
 Query Match 1.9%; Score 31; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 220 TTCCACCCCAATTTATCAAGAAGTCTGAG 250
 |||||
 Db 1 TTCCACCCCAATTTATCAAGAAGTCTGAG 31

RESULT 15
 AAT45757
 ID AAT45757 standard; DNA; 30 BP.
 XX
 XX AAT45757;
 AC AAT45757;
 DT 17-FEB-1997 (first entry)
 XX
 DE Human interleukin-8 gene probe.
 XX
 KW Polymerase chain reaction; PCR; interleukin; IL; cytokine;
 KW growth factor; animal model; stem cell; haematopoiesis; CD34;
 KW infection; HIV; human immunodeficiency virus; immunomodulator;
 KW immortalise; bone marrow; stromal cell; engraftment; determination;
 KW study; research; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9617627-A2.
 XX
 PD 13-JUN-1996.
 XX
 PF 08-DEC-1995; 95WO-US15986.
 XX
 XX 09-DEC-1994; 94US-0352957.
 XX
 XX (GART/) GARTNER S.
 PA (HALL/) HALL E.
 PA (KAUS/) KAUSHAL S.
 PA (KESS/) KESSLER S.
 PA (LRUS/) LA RUSSA V.
 PA (MOSC/) MOSCA J D.
 XX
 PI Gartner S, Hall E, Kaushal S, Kessler S, La Russa V;
 PI Mosca JD;
 XX
 DR WPI; 1996-286928/29.
 XX
 XX Animal models for human haematopoiesis - have en-grafted human or
 PT primate stem cells in the presence of immortalised bone marrow
 PT stromal cells
 XX
 PS Example 1; Page 15; 43pp; English.
 XX
 CC AAT45754-T45762 are probes used to determine whether or not the
 CC cytokines IL-1, IL-6, IL-8, GM-CSF, G-CSF, M-CSF, TGF-alpha and
 CC stem cell factor are expressed by a human bone marrow stromal
 CC cell line, Lof(11-10). The cells were found to produce the cytokines
 CC which support the growth of CD34+ stem cells. The Lof(11-10) cells
 CC were injected into SCID mice (previously irradiated to provide an
 CC internal space for CD34+ cells to populate). Five to seven days
 CC after injection the mice were injected with 3 to 5 human CD34+ cells.
 CC After 3 weeks, human CD34+ cells were found in the bone marrow of
 CC the mice. The immortalised bone marrow stem cells create a human
 CC microenvironment supplying human cytokines in the animals to provide
 CC for the engraftment, maintenance and differentiation of CD34+ stem
 CC cells. Animal models created by administering Lof(11-10) cells are
 CC used to study and determine the effectiveness of therapies against
 CC disease such as HIV infection. They can also be used to assay for
 CC haematopoietic growth factors, immunomodulators and/or immune
 CC toxins.

PN WO9822578-A1.
XX
PD 28-MAY-1998.
XX
XX 12-NOV-1997; 97WO-JP04126.
PF
XX 15-NOV-1996; 96JP-0305163.
PR
XX (CYTO-) INST CYTOSIGNAL RES INC.
PA
XX Nagasawa Y, Yoshida H;
PI
XX WPI; 1998-312464/27.
DR
XX
XX Test system for detecting intra-cellular signal transmission
PT inhibition - using vector containing apoptosis-inhibiting or
PT reporter gene and promoter sequence, used for, e.g. screening for
PT potential anti-inflammatory agents
XX
XX Example 1; Page 20; 62pp; Japanese.
PS
XX PCR primers AAV35780-81 are used in the course of the invention. The
CC specification describes plasmid vectors which comprise a gene which
CC can induce apoptosis under specific conditions, e.g. guanine
CC phosphoribosyltransferase (gpt), or a reporter gene, e.g. luciferase,
CC where the gene is situated downstream of a promoter which responds to
CC specific extracellular stimulation such as the presence of a cytokine,
CC e.g. tumour necrosis factor (TNF) or interleukin-1. The vector may be
CC used to transform a suitable cell line, such as a cell line which does
CC not produce hypoxanthine-guanine phosphoribosyl transferase (HGPRT). The
CC transformed cells are used to test the inhibitory effect of a gene or
CC substance on intracellular signal transmission.
XX
XX Sequence 30 BP; 3 A; 7 C; 8 G; 12 T; 0 other;
SQ
Query Match 1.8%; Score 30; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GACAGCAGAGCAGACACAAAGCTTCTAGGACAA 43
DB 30 GACAGCAGAGCAGACACAAAGCTTCTAGGACAA 1
RESULT 19
AAC88174/c
ID AAC88174 standard; DNA; 30 BP.
XX
AC AAC88174;
XX
DT 14-MAR-2001 (first entry)
XX
XX Human interleukin 8 5'-regulatory sequence PCR primer SEQ ID NO:3.
DE
XX Human; interleukin 8; IL-8; regulation; point mutation; NF-kappa B;
KW AP-1 binding site; interleukin 1 beta; tumour necrosis factor alpha;
KW promoter; antiinflammatory; antiarteriosclerotic; screening; inhibitor;
KW identification; inflammation; arteriosclerosis; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200071697-A1.
PN
XX 30-NOV-2000.
PD
XX 24-MAY-2000; 2000WO-JP03326.
PF
XX 24-MAY-1999; 99JP-0143032.
PR
XX (SANY) SANKYO CO LTD.
PA
XX Koishi R, Yoshimura C, Serizawa N;
XX
XX

DR WPI; 2001-112080/12.
XX
XX Screening for potential inhibitors of the NF-kappa-B activation
PT pathway, useful for treatment of inflammation and arteriosclerosis
XX
XX Example 1; Page 15; 49pp; Japanese.
PS
XX The present invention describes a method for screening for potential
CC specific inhibitors of pathways activated by interleukin (IL)-1 beta,
CC tumour necrosis factor (TNF) alpha or a leustrodaxin derivative, by
CC culturing a cell transformed by a marker gene controlled by a promoter
CC gene containing a NF-kappa-B binding site in the presence of
CC IL1beta/TNFalpha/leustrodaxin derivative and the inhibitor and observing
CC the degree of marker gene expression. Also described is a method for
CC activating a promoter gene containing a NF-kappa-B binding site and
CC inhibitors identified by the above method. The method can be used for
CC the identification of inhibitors of the NF-kappa-B activation pathway
CC which can be used for the treatment of inflammation and arteriosclerosis.
CC The present sequence represents a PCR primer for the 5'-regulatory
CC sequence of the human IL-8 gene, which is used in an example from the
CC present invention.
XX
XX Sequence 30 BP; 3 A; 7 C; 8 G; 12 T; 0 other;
SQ
Query Match 1.8%; Score 30; DB 22; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GACAGCAGAGCAGACACAAAGCTTCTAGGACAA 43
DB 30 GACAGCAGAGCAGACACAAAGCTTCTAGGACAA 1
RESULT 20
ABL46338/c
ID ABL46338 standard; DNA; 30 BP.
XX
AC ABL46338;
XX
XX 26-APR-2002 (first entry)
DT
XX Human interleukin-1 beta oligonucleotide SEQ ID NO:305.
DE
XX Nucleic acid accessible hybridisation site; detection; hybridisation;
KW characterisation; identification; nucleic acid structure; diagnosis;
KW PCR primer; probe; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO200198537-A2.
PN
XX 27-DEC-2001.
PD
XX 15-JUN-2001; 2001WO-US19401.
PF
XX 17-JUN-2000; 2000US-212308P.
PR
XX 15-JUN-2001; 2001US-0212308.
PR
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
PA
XX Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
XX WPI; 2002-049698/06.
PI
XX Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises
PT identifying primers that interact with the target to form an extension
PT product under amplification conditions -
XX
XX Claim 48; Fig 81A; 409pp; English.
PS
XX The present invention describes a method for identifying oligonucleotides
CC

CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention.

XX
SQ Sequence 30 BP; 13 A; 4 C; 2 G; 11 T; 0 other;

Query Match 1.8%; Score 30; DB 24; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1165 ATGATGTTTTATTAGATAAAATTTCAATCAG 1194

Db 30 ATGATGTTTTATTAGATAAAATTTCAATCAG 1

Search completed: February 9, 2003, 17:30:46
Job time : 350 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 15:52:56 ; Search time 4173 Seconds
(without alignments)
11430.505 Million cell updates/sec

Title: US-09-960-143-3
Perfect score: 1639
Sequence: 1 acaacttcagagacagca.....atataattgtgtcaagt 1639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	37.4	2.3	47	6	AR021184	AR021184 Sequence
2	37.4	2.3	47	6	I60565	I60565 Sequence 42
C 3	37	2.3	47	6	AR021182	AR021182 Sequence
C 4	37	2.3	37	6	I60563	I60563 Sequence 40
C 5	33	2.0	33	6	A56958	A56958 Sequence 16
C 6	33	2.0	33	6	AR052918	AR052918 Sequence
C 7	33	2.0	33	6	AR054281	AR054281 Sequence
C 8	33	2.0	33	6	AR054483	AR054483 Sequence
C 9	30.6	1.9	31	6	AX249279	AX249279 Sequence
C 10	30	1.8	30	6	AR200024	AR200024 Sequence
C 11	30	1.8	30	6	AX419968	AX419968 Sequence
C 12	30	1.8	30	6	BD004257	BD004257 Method fo
C 13	29	1.8	29	6	AX317616	AX317616 Sequence
C 14	28	1.7	28	6	AR090359	AR090359 Sequence
C 15	28	1.7	28	6	AR090360	AR090360 Sequence
C 16	28	1.7	28	6	AR197394	AR197394 Sequence
C 17	28	1.7	28	6	AR197395	AR197395 Sequence
C 18	26	1.6	26	6	AX280042	AX280042 Sequence
C 19	25	1.5	25	6	I22270	I22270 Sequence 8
C 20	25	1.5	26	6	AX280041	AX280041 Sequence
C 21	24	1.5	24	6	AR207732	AR207732 Sequence
C 22	23	1.4	23	6	I22269	I22269 Sequence 7
C 23	23	1.4	40	6	AR021188	AR021188 Sequence
C 24	22.8	1.4	31	6	AX203829	AX203829 Sequence
C 25	22.8	1.4	48	6	AX426642	AX426642 Sequence
C 26	22.6	1.4	48	6	AX426920	AX426920 Sequence
C 27	22.2	1.4	28	6	AX203828	AX203828 Sequence
C 28	22	1.3	22	6	AR130451	AR130451 Sequence
C 29	22	1.3	22	6	E09226	E09226 Primer for
C 30	22	1.3	22	6	E09227	E09227 Primer for
C 31	22	1.3	48	6	I33522	I33522 Sequence 1
C 32	22	1.3	50	8	CNS018YM	AL110965 Botrytis
C 33	21.8	1.3	47	6	AX114372	AX114372 Sequence
C 34	21.8	1.3	48	6	I33523	I33523 Sequence 2
C 35	21.6	1.3	41	6	AR164944	AR164944 Sequence
C 36	21.6	1.3	41	6	E22883	E22883 DNA sequenc
C 37	21.6	1.3	50	6	AX160081	AX160081 Sequence
C 38	21.6	1.3	50	6	AX160578	AX160578 Sequence
C 39	21.4	1.3	43	6	AX484483	AX484483 Sequence
C 40	21.4	1.3	47	1	LACDRRH	M84772 Lactococcus
C 41	21.4	1.3	48	9	S64862S2	S64863 alpha 1-the
C 42	21.2	1.3	43	6	AX484516	AX484516 Sequence
C 43	21.2	1.3	45	8	AB008098	AB008098 Saccharom
C 44	21.2	1.3	50	6	AX157057	AX157057 Sequence
C 45	21	1.3	21	6	A56957	A56957 Sequence 15

ALIGNMENTS

RESULT 1
AR021184
LOCUS AR021184 47 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 42 from patent US 5789539.
ACCESSION AR021184
VERSION AR021184.1 GI:3975799
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Daly,T.J. and Larosa,G.J.
TITLE Chemokine-like proteins and methods of use
JOURNAL Patent: US 5789539-A 42 04-AUG-1998;
FEATURES Location/Qualifiers

RESULT 4

TITLE Use of interleukin-10 (IL-10) to treat endotoxin- or superantigen-induced toxicity

JOURNAL Patent: US 5833976-A 42 10-NOV-1998;

FEATURES Location/Qualifiers

source 1..33

BASE COUNT 9 a 10 c 2 g 12 t

ORIGIN

Query Match

Best Local Similarity 2.0%; Score 33; DB 6; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAACTTTTGAAGAGGGCTGAGAATTCATAA 390

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Db 33 GAGAACTTTTGAAGAGGGCTGAGAATTCATAA 1

RESULT 7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BASE COUNT

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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||

Db 33 GAGAACTTTTGAAGAGGGCTGAGAATTCATAA 1

RESULT 8

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 2.0%; Score 33; DB 6; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TITLE Use of interleukin-10 (IL-10) to treat endotoxin- or superantigen-induced toxicity

JOURNAL Patent: US 5833976-A 42 10-NOV-1998;

FEATURES Location/Qualifiers

source 1..33

BASE COUNT 9 a 10 c 2 g 12 t

ORIGIN

Query Match

Best Local Similarity 2.0%; Score 33; DB 6; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAACTTTTGAAGAGGGCTGAGAATTCATAA 390

|||||

Db 33 GAGAACTTTTGAAGAGGGCTGAGAATTCATAA 1

RESULT 7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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Query Match

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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

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ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 2.0%; Score 33; DB 6; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TITLE Use of interleukin-10 (IL-10) to treat endotoxin- or superantigen-induced toxicity

JOURNAL Patent: US 5833976-A 42 10-NOV-1998;

FEATURES Location/Qualifiers

source 1..33

BASE COUNT 9 a 10 c 2 g 12 t

ORIGIN

Query Match

Best Local Similarity 2.0%; Score 33; DB 6; Length 33;

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QY 358 GAGAACTTTTGAAGAGGGCTGAGAATTCATAA 390

|||||

Db 33 GAGAACTTTTGAAGAGGGCTGAGAATTCATAA 1

RESULT 7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8

LOCUS

DEFINITION

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VERSION

KEYWORDS

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ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 2.0%; Score 33; DB 6; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AX419968.1 GI:21524335
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE
Nucleic acid accessible hybridization sites
JOURNAL
Patent: WO 0198537-A 305 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
Location/Qualifiers
1..30
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BASE COUNT 13 a 4 c 2 g 11 t
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Db 30 ATGATGTTTATTAGATAAATTTCAATCAG 1
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RESULT 12
BD004257/c
LOCUS 30 bp DNA linear PAT 31-JAN-2002
DEFINITION
Method for searching physiologically active substance.
ACCESSION
BD004257
VERSION
JP 2001037492-A/3.
KEYWORDS
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Koishi,R., Yoshimura,C. and Serizawa,N.
TITLE
Method for searching physiologically active substance
JOURNAL
Patent: JP 2001037492-A 3 13-FEB-2001;
COMMENT
SANKYO CO LTD
OS Artificial Sequence
PN JP 2001037492-A/3
PD 13-FEB-2001
PF 24-MAY-2000 JP 2000152282
PR
PI RYUTA KOISHI,CHIGUSA YOSHIMURA,NOBUKI SERIZAWA PC
C12N15/09,C12N5/10,C12N15/00,C12N5/00 CC
FH Key Location/Qualifiers
FT source 1..30
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FEATURES
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Location/Qualifiers
1..30
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Qy 14 GACAGCAGACACACAGCTTCTAGGACAA 43
|||||
Db 30 GACAGCAGACACACAGCTTCTAGGACAA 1
|||||
RESULT 13
AX317616/c
LOCUS 29 bp DNA linear PAT 14-DEC-2001
DEFINITION
Sequence 619 from Patent WO0190337.
ACCESSION
AX317616
VERSION
AX317616.1 GI:17900517

AX419968.1 GI:21524335
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE
Nucleic acid accessible hybridization sites
JOURNAL
Patent: WO 0198537-A 305 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
Location/Qualifiers
1..30
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ORIGIN
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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 30 ATGATGTTTATTAGATAAATTTCAATCAG 1
|||||
RESULT 12
BD004257/c
LOCUS 30 bp DNA linear PAT 31-JAN-2002
DEFINITION
Method for searching physiologically active substance.
ACCESSION
BD004257
VERSION
JP 2001037492-A/3.
KEYWORDS
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Koishi,R., Yoshimura,C. and Serizawa,N.
TITLE
Method for searching physiologically active substance
JOURNAL
Patent: JP 2001037492-A 3 13-FEB-2001;
COMMENT
SANKYO CO LTD
OS Artificial Sequence
PN JP 2001037492-A/3
PD 13-FEB-2001
PF 24-MAY-2000 JP 2000152282
PR
PI RYUTA KOISHI,CHIGUSA YOSHIMURA,NOBUKI SERIZAWA PC
C12N15/09,C12N5/10,C12N15/00,C12N5/00 CC
FH Key Location/Qualifiers
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FT /organism="Artificial Sequence".
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Location/Qualifiers
1..30
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/db_xref="taxon:32630"
BASE COUNT 3 a 7 c 8 g 12 t
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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 GACAGCAGACACACAGCTTCTAGGACAA 43
|||||
Db 30 GACAGCAGACACACAGCTTCTAGGACAA 1
|||||
RESULT 13
AX317616/c
LOCUS 29 bp DNA linear PAT 14-DEC-2001
DEFINITION
Sequence 619 from Patent WO0190337.
ACCESSION
AX317616
VERSION
AX317616.1 GI:17900517

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Allawi,H., Bartholomay,C.T., Chehak,L., Curtis,M.L., Els,P.S.,
Hall,J.G., Ip,H.S., Kaiser,M., Kwiatkowski,R.W., Lukowiak,A.A.,
Lyamichev,V., Ma,W., Olson-Munoz,M.C., Olson,S.M., Schaefer,J.J.,
Strzypczynski,Z., Takova,T.Y., Vedvik,K.L. and Lyamichev,N.E.
TITLE
Detection of rna
JOURNAL
Patent: WO 0190337-A 619 29-NOV-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
Location/Qualifiers
1..29
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BASE COUNT 8 a 0 c 11 g 10 t
ORIGIN
Query Match 1.8%; Score 29; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 211 TCCAAACCTTTCCACCCCAAAATTTATCAA 239
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Db 29 TCCAAACCTTTCCACCCCAAAATTTATCAA 1
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RESULT 14
AR090359
LOCUS 28 bp DNA linear PAT 07-SEP-2000
DEFINITION
Sequence 479 from patent US 5994076.
ACCESSION
AR090359
VERSION
AR090359.1 GI:10017114
KEYWORDS
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 28)
AUTHORS
Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE
Methods of assaying differential expression
JOURNAL
Patent: US 5994076-A 479 30-NOV-1999;
FEATURES
Location/Qualifiers
1..28
/organism="unknown"
BASE COUNT 6 a 9 c 7 g 6 t
ORIGIN
Query Match 1.7%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.8e+05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 88 AACATGACTTCCAAGCTGCCGTGGCTC 115
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Db 1 AACATGACTTCCAAGCTGCCGTGGCTC 28
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RESULT 15
AR090360/c
LOCUS 28 bp DNA linear PAT 07-SEP-2000
DEFINITION
Sequence 480 from patent US 5994076.
ACCESSION
AR090360
VERSION
AR090360.1 GI:10017115
KEYWORDS
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 28)
AUTHORS
Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE
Methods of assaying differential expression
JOURNAL
Patent: US 5994076-A 480 30-NOV-1999;
FEATURES
Location/Qualifiers
1..28
source

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LOCUS AX280042 Sequence 17 from Patent WO0177382. 26 bp DNA linear PAT 02-NOV-2001
DEFINITION
ACCESSION AX280042
VERSION AX280042.1 GI:16607493
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Hull, J. and Kwiatkowski, D.P.
TITLE Genetic factor affecting cytokine expression
JOURNAL Patent: WO 0177382-A 17 18-OCT-2001;
FEATURES
SOURCE Location/Qualifiers
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            /db_xref="taxon:32630"
            /note="Oligonucleotide"
BASE COUNT 9 a 5 c 2 g 10 t
ORIGIN

Query Match 1.6%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1228 CCCAGTTAAATTTTCATTTTCAGATAA 1253
Db 1 CCCAGTTAAATTTTCATTTTCAGATAA 26

RESULT 19
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LOCUS I22270 Sequence 8 from patent US 5527678. 25 bp DNA linear PAT 07-OCT-1996
DEFINITION
ACCESSION I22270
VERSION I22270.1 GI:1602624
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Blaser, M.J., Tummuru, M.K.R. and Sharma, S.A.
TITLE CagB and CagC genes of helicobacter pylori and related compositions
JOURNAL Patent: US 5527678-A 8 18-JUN-1996;
FEATURES
SOURCE Location/Qualifiers
          1..25
            /organism="unknown"
BASE COUNT 6 a 10 c 1 g 8 t
ORIGIN

Query Match 1.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGAAGTTTTTGAAGAGGCGTGAGA 382
Db 25 GAGAAGTTTTTGAAGAGGCGTGAGA 1

RESULT 20
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LOCUS AX280041 Sequence 16 from Patent WO0177382. 26 bp DNA linear PAT 02-NOV-2001
DEFINITION
ACCESSION AX280041
VERSION AX280041.1 GI:16607492
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Hull, J. and Kwiatkowski, D.P.
TITLE Genetic factor affecting cytokine expression
JOURNAL Patent: WO 0177382-A 16 18-OCT-2001;

LOCUS AX280042 Sequence 17 from Patent WO0177382. 26 bp DNA linear PAT 02-NOV-2001
DEFINITION
ACCESSION AX280042
VERSION AX280042.1 GI:16607493
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Hull, J. and Kwiatkowski, D.P.
TITLE Genetic factor affecting cytokine expression
JOURNAL Patent: WO 0177382-A 17 18-OCT-2001;
FEATURES
SOURCE Location/Qualifiers
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            /organism="synthetic construct"
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            /note="Oligonucleotide"
BASE COUNT 9 a 5 c 2 g 10 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.8e+05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 GAGTGATTGAGAGTGACACACTGCGC 275
Db 28 GAGTGATTGAGAGTGACACACTGCGC 1

RESULT 16
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LOCUS AR197394 Sequence 479 from patent US 6352829. 28 bp DNA linear PAT 20-APR-2002
DEFINITION
ACCESSION AR197394
VERSION AR197394.1 GI:20247243
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 479 05-MAR-2002;
FEATURES
SOURCE Location/Qualifiers
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            /organism="unknown"
BASE COUNT 6 a 9 c 7 g 6 t
ORIGIN

Query Match 1.7%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.8e+05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 AACATGACTTCCAAGTGGCGGTGCTC 115
Db 1 AACATGACTTCCAAGTGGCGGTGCTC 28

RESULT 17
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LOCUS AR197395 Sequence 480 from patent US 6352829. 28 bp DNA linear PAT 20-APR-2002
DEFINITION
ACCESSION AR197395
VERSION AR197395.1 GI:20247244
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 480 05-MAR-2002;
FEATURES
SOURCE Location/Qualifiers
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ORIGIN

Query Match 1.7%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.8e+05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 GAGTGATTGAGAGTGACACACTGCGC 275
Db 28 GAGTGATTGAGAGTGACACACTGCGC 1

RESULT 18
AX280042
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FEATURES ISIS INNOVATION LIMITED (GB)
 Location/Qualifiers
 source 1. .26
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Oligonucleotide"
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 ORIGIN

Query Match 1.5%; Score 25; DB 6; Length 26;
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 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1228 CCCAGTTAAATTTTCATTCAGATA 1252
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